

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Levy, Gary
- (ii) TITLE OF INVENTION: Methods of Modulating Immune Coagulation
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: BERESKIN & PARR
 - (B) STREET: 40 King Street West
 - (C) CITY: Toronto
 - (D) STATE: Ontario
 - (E) COUNTRY: Canada
 - (F) ZIP: M5H 3Y3
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Gravelle, Micheline
 - (B) REGISTRATION NUMBER: 40,261
 - (C) REFERENCE/DOCKET NUMBER: 9579-006
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (416) 364-7311
 - (B) TELEFAX: (416) 361-1398

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4630 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GATCTAGGGT TGGAAGCCAG GTCTCCTGAG TATGCGAGAA TAAATACAGT CATGGAAGTG	60
TAAAGAGTCT GCCAACATTT TGAGAATGTG AATAGGATTT GGCTAAAATT AAGGGGATAT	120
ACAGAAAAGT CATAGGAAAT CAGGTTAAAG ACATAAATAT GAGATAGGCT ACAGAGTGTT	180
TTAAGTAATA CAATAAAACA TTTAGATTT TGCCCATGTC AGTCATTTG AAATTATTTT	240
TAAAGCAAAA AAACCCCTTT TAAACAAAGAA ATCTTATGAG ATGTCAATAT GCAAAACAAA	300
TTAAAAGGAG GTGGTTTCTC TAACTGAAGC TGTTCCCTCTT TCCTGCCTTC AGCCTCTGAA	360

GAGAAAGTTA GAAAACATT ATTACATTAATG CTACATGTTT TGAACAAAGCT GATATAACAA 420
GTGGCCCAGA GAGCAGGTAG AAGAACCCAGC GTGGAGACAG AAAGCAAGAG GCCCGCCTGC 480
CAGGGCTACC TGCAGAAAGA AAGGGCAAAG ATGCTGTAGG CAAGAGAAAGT TCAGGACAGA 540
CACTGGCATA GCTCAAAGAT TCACATTGAG GCAGCTGTGG AAGATGACAG TACAATTACC 600
AAAATGTCGA AGGGCAAAGG AGGCAGCTAC TGGTTTGAT GAAAGACAAT TATGTCCTTT 660
TAAATGGGTC TTAGACATTT AGACATTTAT ATACACTATG CTACGGACAA AGGAATAGAA 720
AGTAGCACTT TTTCTCCAC TAGTTTCTT CTCTTTTCA AGTAGATGAA GCAAAAGTCA 780
ACTGCAATAG TCAGAAAGCT GTACTTTGTT ACACCTAGAA ACTTCTAAAA GTGCTTAAGA 840
TTTCACCTGA AAGTCCAACA TGAAGAAAAT ACAGGCTCCC CAATGCCCA TTCTAAGAAG 900
GAAAAAGGAC CATTTCATT TTAGTAACGT TTCTGTTCTA TAGACAGTTT GGATAACTAG 960
CTCTTACTTT TTATCTTTAA AAACTGTTT TCCAGTGAAG TTACGTATAA TTATTTACTT 1020
CAAGCGTAGT ATACCAAATT ACTTTAGAAA TGCAAGACTT TTCTTATACT TCATAAAAATA 1080
CATTATGAAA GTGAATCTTG TTGGCTGTGT ACATTTGACT ATAATAATTT CAATGCATAT 1140
TATTTCTATT GAGAGTAAGT TACAGTTTT GGCAAACCTGC GTTTGATGAG GGCTATCTCC 1200
TCTTCCTGTG CGTTTCTAAA ACTTGTGATG CAAACGCTCC CACCCTTCC TGGGAACACA 1260
GAAAGCCTGA CTCAGGCCAT GGCGCTATT AAAGCAGCTC CAGCCCTGCG CACTCCCTGC 1320
TGGGGTGAGC AGCACTGTAA AGATGAAGCT GGCTAACTGG TACTGGCTGA GCTCAGCTGT 1380
TCTTGCCACT TACGGTTTT TGTTGTGGC AAACAATGAA ACAGAGGAAA TTAAAGATGA 1440
AAGAGCAAAG GATGTCTGCC CAGTGAGACT AGAAAGCAGA GGGAAATGCG AAGAGGCAGG 1500
GGAGTGCCCC TACCAGGTAA GCCTGCCCTT CTTGACTATT CAGCTCCGA AGCAATTCAAG 1560
CAGGATCGAG GAGGTGTTCA AAGAAGTCCA AACCTCAAG GAAATCGTAA ATAGTCTAAA 1620
GAAATCTTGC CAAGACTGCA AGCTGCAGGC TGATGACAAC GGAGACCCAG GCAGAAACGG 1680
ACTGTTGTTA CCCAGTACAG GAGCCCCGGG AGAGGTTGGT GATAACAGAG TTAGAGAATT 1740
AGAGAGTGAG GTTAACAAGC TGTCCTCTGA GCTAAAGAAT GCCAAAGAGG AGATCAATGT 1800
ACTTCATGGT CGCCTGGAGA AGCTGAATCT TGTAAATATG AACAAACATAG AAAATTATGT 1860
TGACAGCAAA GTGGCAAATC TAACATTGT TGTCAATAGT TTGGATGGCA AATGTTCAAA 1920
GTGTCCCAGC CAAGAACAAA TACAGTCACG TCCAGGTATG TATAATAATG TTTTCTTATC 1980
ATATGTTCAT AAATGTTATA CAGTCAGAGA TGTATCTAAA AGATTAACCT GAGTCAGTAA 2040
GTTAAATAGA TGACAGATTA AGTCTTTAT TTATCAAGGT GCACAGGAAA AAATAAATAT 2100
CTTCTCAAAT ATGACCACAT AAATATGACC TAATTACAAA ATCATAGTTA GTTCTGTATC 2160
CACTGGAAGT CACTTTCAAT TTTAAGATCT TATTTGTTAA TGCCAGACCT ACTTGCAAGC 2220
AGAGATTAGA GGTCTTTCT GCTTTATAAC ATTAGGTTCT PCTTGTGAGG CCTTAAGCAT 2280
TTACTAAACA CCTTCAAGTA AGTTTAGTAA AGTTTCATTA CTGCCATTGA TTCAATTATC 2340

AAACTGCTTT	TGTACATATA	AAGAATTCTT	CAGATGCATG	GTTTCTATT	ACAAGATCCA	2400
ATGCCTTCCT	TTTATTTCCC	CTTCAGTTCA	ACATCTAATA	TATAAAGATT	GCTCTGACTA	2460
CTACGCAATA	GGCAAAAGAA	GCAGTGAGAC	CTACAGAGTT	ACACCTGATC	CCAAAAATAG	2520
TAGCTTGAA	GTTTACTGTG	ACATGGAGAC	CATGGGGGA	GGCTGGACAG	TGCTGCAGGC	2580
ACGTCTCGAT	GGGAGCACCA	ACTTCACCAG	AACATGGCAA	GACTACAAAG	CAGGCTTGG	2640
AAACCTCAGA	AGGGAATTT	GGCTGGGGAA	CGATAAAATT	CATCTTCTGA	CCAAGAGTAA	2700
GGAAATGATT	CTGAGAATAG	ATCTTGAAGA	CTTTAATGGT	GTCGAACAT	ATGCCTTGTA	2760
TGATCAGTT	TATGTGGCTA	ATGAGTTCT	CAAATATCGT	TTACACGTTG	GTAACTATAA	2820
TGGCACAGCT	GGAGATGCAT	TACGTTCAA	CAAACATTAC	AACCACGATC	TGAAGTTTT	2880
CACCACTCCA	GATAAAGACA	ATGATCGATA	TCCTTCTGGG	AACTGTGGC	TGTACTACAG	2940
TTCAGGCTGG	TGGTTTGATG	CATGTCTTC	TGCAAACCTA	AATGGCAAAT	ATTATCACCA	3000
AAAATACAGA	GGTGTCCGTA	ATGGGATTT	CTGGGGTACC	TGGCCTGGTG	TAAGTGAGGC	3060
ACACCCCTGGT	GGCTACAAGT	CCTCCTTCAA	AGAGGCTAAG	ATGATGATCA	GACCCAAGCA	3120
CTTTAAGCCA	TAAATCACTC	TGTTCATTCC	TCCAGGTATT	CGTTATCTAA	TAGGGCAATT	3180
AATTCCATTGT	TTCATATT	TCATAGCTAA	AAAATGATGT	CTGACGGCTA	GGTTCTTATG	3240
CTACACAGCA	TTTGAAATAA	AGCTGAAAAA	CAATGCATTT	TAAAGGAGTC	CTTTGTTGTT	3300
ATGCTGTTAT	CCAATGAACA	CTTGCAAGCA	ATTAGCAATA	TTGAGAATTA	TACATTAGAT	3360
TTACAATTCT	TTTAATTCT	ATTGAAACTT	TTTCTATTGC	TTGTATTACT	TGCTGTATTT	3420
AAAAAAATAAT	TGTTGGCTGG	GTGTGGTAGC	TCACGCCGT	AATCCCAGCA	CTTTGGAATG	3480
TCAAGGCAGG	CAGATCACTT	GAGGTCAAGGA	GTTTGAGACC	AGCCTGGCCA	AACATGTGAA	3540
ACGCTGTCTC	TATTAATAAAT	ACAAAAATTA	GCCGGGCATG	GTGGTACATG	CCTGTAATCA	3600
ACGCTGTTA	TTAAAAATAC	AAAAATTAGC	CGGGCATGGT	GGACATGCCT	GTAATCCTAG	3660
TACTTGGGAG	GCTGAGGCAG	GAGAATCGCT	TGAACCTGAG	AGGAAGAGGT	TGCAGTGAGC	3720
CAAGAATGAG	CCACTGCACT	CCAGCATGGG	TGACAGAGAA	AACTCTGTCT	CAAACAAAAA	3780
AATAATAAAA	TTTATTCACT	AGGTGGATTC	TACACAAAGT	AATCTGTATT	TGGGCCATGA	3840
TTTAAGCACA	TCTGAAGGTA	TATCACTCTT	TTCAGGCTAT	AATTATTGG	GTAATCTTCA	3900
TTCTGAGACA	AACTTAATCT	ATATCATT	CTTGCAACA	GAACAACCT	ACAGCATT	3960
GGTTCCCAGA	CTAAGGGAAC	TAATATCTAT	ATAATTAAAC	TTGTTCATTT	ATCATTGATG	4020
AAATATAAAA	TACTTGTCA	TTAAACCGTT	AAAAAATGTG	GTAGCATAAT	GTCACCCCAA	4080
AAAGCATTCA	GAAAGCAATG	TAACTGTGAA	GACCAGGGTT	TAAAGGTAAT	TCATTTATAG	4140
TTTATAACTC	CTTAGATGTT	TGATGTTGAA	AACTGCTTA	ACATGAAAAT	TATCTCCTC	4200
TGCTCTGTGT	GAACAATAGC	TTTAATT	AGATTGCTCA	CTACTGTACT	AGACTACTGG	4260
TAGGTTTTT	TGGGGGGGGG	TGGTAGGGA	TATGTGGGTA	ATGAAGCATT	TACTTACAGG	4320

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CTATCATACT CTGAGGCCAA TTTTATCTCC AAAGCAATAA TATCATTAAAG TGATTCAC	4380
CATAGAAGGC TAAGTTTCTC TAGGACAGAT AGAAAACATG AATTTGAAA TATATAGAAC	4440
AGTAGTTAAA ATACTATATA TTTCAACCCT GGCTGGTAGA TTGCTTATT TACTATCAGA	4500
AACTAAAAGA TAGATTTTA CCCAACAGA AGTATCTGTA ATTTTATAA TTCATCAATT	4560
CTGGAATGCT ATATATAATA TTTAAAAGAC TTTTAAATG TGTTTAATT CATCATCGTA	4620
AAAAGGGATC	4630

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys Leu Ala Asn Trp Tyr Trp Leu Ser Ser Ala Val Leu Ala Thr	
1 5 10 15	
Tyr Gly Phe Leu Val Val Ala Asn Asn Glu Thr Glu Glu Ile Lys Asp	
20 25 30	
Glu Arg Ala Lys Asp Val Cys Pro Val Arg Leu Glu Ser Arg Gly Lys	
35 40 45	
Cys Glu Glu Ala Gly Glu Cys Pro Tyr Gln Val Ser Leu Pro Pro Leu	
50 55 60	
Thr Ile Gln Leu Pro Lys Gln Phe Ser Arg Ile Glu Glu Val Phe Lys	
65 70 75 80	
Glu Val Gln Asn Leu Lys Glu Ile Val Asn Ser Leu Lys Ser Cys	
85 90 95	
Gln Asp Cys Lys Leu Gln Ala Asp Asp Asn Gly Asp Pro Gly Arg Asn	
100 105 110	
Gly Leu Leu Leu Pro Ser Thr Gly Ala Pro Gly Glu Val Gly Asp Asn	
115 120 125	
Arg Val Arg Glu Leu Glu Ser Glu Val Asn Lys Leu Ser Ser Glu Leu	
130 135 140	
Lys Asn Ala Lys Glu Glu Ile Asn Val Leu His Gly Arg Leu Glu Lys	
145 150 155 160	
Leu Asn Leu Val Asn Met Asn Asn Ile Glu Asn Tyr Val Asp Ser Lys	
165 170 175	
Val Ala Asn Leu Thr Phe Val Val Asn Ser Leu Asp Gly Lys Cys Ser	
180 185 190	
Lys Cys Pro Ser Gln Glu Gln Ile Gln Ser Arg Pro Val Gln His Leu	
195 200 205	
Ile Tyr Lys Asp Cys Ser Asp Tyr Tyr Ala Ile Gly Lys Arg Ser Ser	
210 215 220	

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Glu Thr Tyr Arg Val Thr Pro Asp Pro Lys Asn Ser Ser Phe Glu Val
 225 230 235 240
 Tyr Cys Asp Met Glu Thr Met Gly Gly Gly Trp Thr Val Leu Gln Ala
 245 250 255
 Arg Leu Asp Gly Ser Thr Asn Phe Thr Arg Thr Trp Gln Asp Tyr Lys
 260 265 270
 Ala Gly Phe Gly Asn Leu Arg Arg Glu Phe Trp Leu Gly Asn Asp Lys
 275 280 285
 Ile His Leu Leu Thr Lys Ser Lys Glu Met Ile Leu Arg Ile Asp Leu
 290 295 300
 Glu Asp Phe Asn Gly Val Glu Leu Tyr Ala Leu Tyr Asp Gln Phe Tyr
 305 310 315 320
 Val Ala Asn Glu Phe Leu Lys Tyr Arg Leu His Val Gly Asn Tyr Asn
 325 330 335
 Gly Thr Ala Gly Asp Ala Leu Arg Phe Asn Lys His Tyr Asn His Asp
 340 345 350
 Leu Lys Phe Phe Thr Thr Pro Asp Lys Asp Asn Asp Arg Tyr Pro Ser
 355 360 365
 Gly Asn Cys Gly Leu Tyr Tyr Ser Ser Gly Trp Trp Phe Asp Ala Cys
 370 375 380
 Leu Ser Ala Asn Leu Asn Gly Lys Tyr Tyr His Gln Lys Tyr Arg Gly
 385 390 395 400
 Val Arg Asn Gly Ile Phe Trp Gly Thr Trp Pro Gly Val Ser Glu Ala
 405 410 415
 His Pro Gly Gly Tyr Lys Ser Ser Phe Lys Glu Ala Lys Met Met Ile
 420 425 430
 Arg Pro Lys His Phe Lys Pro
 435

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5403 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CATAAGGC GTCTGACAAA TTCTTCATAC ACACATTCC CCTTGACACA TTCA GTCTGT	60
ATAGGTTATT TCTATAGGAG AAAAAAAATA TTCAAATTCC TTGTGCCTG GTAACAGGCA	120
TGAAGGCTCA GCAAAGCCAA TACGTGTTAT GTCCAGTTGG AGACAGTGCC AGGGCCAACA	180
TTCCAGACTT CTCAGATAGA AAGTGCCT GCCTGCCCTG CTCTGAGAAT TTGAAGAGAG	240
TAGTCAGTT AGAATTAAGA GGCAGTAGAG AAAAGTCTTG GGAAATCTGG TTAGAGATAT	300
AAATATGAGA ACTGGACATG GTGGTACACA CCTGTGATCT CTGTGTTAG GAGGGAGAGG	360

CAGAGAGATC AGGAGTTCAA GGCCAGCCTG AGCTACTTGA GACCCAGTCT AAATAAATAA	420
GAGATAGATT ACAGAGTGCC TTTAACTAGT ACAGAGAAAG AATTTGGTT TATCTGTGTC	480
AGTTACGCTG AAATAATTAA TAAGTAATAA AATCCCTTT AATAAGAAAC CTTATGAGGT	540
CAGTATGCAC AATGAACCTA AGAGAGACCC CCAGCTCCTG AGCTGAGTGA TGGGGAAGGA	600
CAGCCACTGC CTGTGATGTG TGAGTGACGT GCTTCCAAGT GTTTAACCA CTGACGATTA	660
CATAGCCTGC ACAGTCAGGA GAAAACAGCC GTATTCTCTG CCAGTTCTCT TCCCTTTAC	720
AAACAGATGA GAGACACACA CAGAGAACATCC ATTTAAAGAG CGGACCTTG TTCTGATTAG	780
GGGCAATTAA AAGTACTTAA GAGTCACAC AAAGTCTAGC CTTCAAAAAG AAAACAGGTT	840
CCCAAACTAG GGAGGAAACA GAATCATTTC CATTGGTG ACATTTAGTG GGAAGAAGCT	900
CACAGACATT TAGACGTTCC AACTCTTCC CCACTAGTGG ACCAAGTATA TAATATGGTA	960
TCTTTGGC ACTGGTATTA CAACTGTTT TTAAACAAAA GACTTCCTT GTGCTTTACT	1020
AAAAAACCCAG ACGGTGAATC TTGAATACAA TGCCTGGCAC CCACGGCAGG CATTCTATTG	1080
TGCATAGTT TGACTGACAG GAGATGACAG CATTGGCTG GCTGCGCTTG CTGAGGACCC	1140
TCTCCTCCTG TGTGGCGTCT GAGACTGTGA TGCAAATGCG CCCGCCCTT TCTGGAACT	1200
CAGAACGCCT GAGTCAGGCG GCGGTGGCTA TTAAAGCGCC TGGTCAGGCT GGGCTGCCGC	1260
ACTGCAAGGA TGAGGCTTCC TGGTTGGTTG TGGCTGAGTT CTGCCGTCT CGCTGCCGTG	1320
CGAGCGGTGG AGGAGCACAA CCTGACTGAG GGGCTGGAGG ATGCCAGGCC CCAGGCTGCC	1380
TGCCCGCGA GGCTGGAGGG CAGCGGGAGG TGCAGGGGA GCCAGTGCC CTTCCAGCTC	1440
ACCCCTGCCCA CGCTGACCAT CCAGCTCCCG CGGCAGCTTG GCAGCATGGA GGAGGTGCTC	1500
AAAGAAGTGC GGACCCCTCAA GGAAGCAGTG GACAGTCTGA AGAAATCCTG CCAGGACTGT	1560
AAGTTGCAGG CTGACGACCA TCGAGATCCC GGCAGGAATG GAGGGATGG AGCAGAGACA	1620
GCCGAGGACA GTAGAGTCCA GGAAGCTGGAG AGTCAGGTGA ACAAGCTGTC CTCAGAGCTG	1680
AAGAATGCAA AGGACCAGAT CCAGGGCTG CAGGGCGCC TGGAGACGCT CCATCTGGTA	1740
AATATGAACA ACATTGAGAA CTACGTGGAC AACAAAGTGG CAAATCTAAC CGTTGTGGTC	1800
AACAGTTGG ATGGCAAGTG TTCCAAGTGT CCCAGCCAAG AACACATGCA GTCACAGCCG	1860
GGTAGGTGTA ATGAGGGTCA TACAGTTGT TCATGAAAGC TGTATGCCA GATAGTGGCC	1920
ATAAACATTA ACCCGAGGGGA GCATAAGTTA GTCAGACTTT CACCTGTTAA GTTATGGCAG	1980
GAGAAACAAG TGTGTTCTCA AATGAGACAA CAGAAATGGT AAATGATCCA CGTACAAAAA	2040
TCCTATTAGT TGTACTCGTT AGAGACCGTC ACTTGCAAGT CTCTAGACCT TCCCTGCTAG	2100
GTGACCAAC AGACGAGCAG AACAGATTC CTCCCGGAAT CTGAACACAT ATTTGAACAC	2160
AGGACAGGTA TGGCAAGGTT CCTGGCTCTG CTTGCTTAGG TCCCTGGAA TCAGATCTG	2220
GGTGGCTGAT GGGCTTATA AGGCTTCAC AAACAATCTG CTGTGCTAGG TTCTCAAATA	2280
TCTAGTGAGA ATGGGAGATT TTTATACATG GAAGCATCTC TCCTCTCTCT CTCCTCTCTC	2340

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ACCTTTGTGG ATGGGTTGCC ACACCCTCTG TGTCATCCT GACTGTGAGG TCGATGGGAC 2640
ATAGTAGGGA TAACTTCAT TTGGAATCTC TAGAGATGGT AGGTCATCAT GTCATAGAAT 2700
GTTATCACTA ATGACCAAGA TAGACACTCA TGTTAAGAG ACATCACAAG GTGTATATTA 2760
AATATGACAT GGCATATAAC TTGTAATGAC ACAAAAATAT TCTGTTACCT ACTTTCTCC 2820
TAAAAGCTTG GGACTCTCCA GAGTTCTAAA TACATGAAA CAGATTATTG TGTTTACAG 2880
GAATCTTATA TTGAACCTTC TTTACCTGAC TCAAATTAA TTAAAATTAA CTGGGAACAA 2940
ATAGTTGGTC TCTAATCTCT ACAAAAACCA CCAAATGATT ACAGTGAGCA TAATTATAAT 3000
CACCTGCTG CTACGTCTAG AAACCAAAC GTGAAATATT GGCTGACTGT ATACCTTCCT 3060
AAATAATAAA TTCAGGATAA CATTGCCATA TTATTGGAGA ACCCCCCCT CCCTTTAAA 3120
ACTGGAATCA TTTTATGTCA ATCTCAGGTG AAATACGAAT GGGTTTCAGA ACAGTGCTGT 3180
GCACTGAAGG CTGACATTAA GAACATATAT AACGATTCT GTAAAGTCTG CTGTAACAAT 3240
TGCTGATTGT ATCCTAGGAG ACTTGGACTC CTCTCAACGT TAAGGCAGAG GAATATAATG 3300
GTTATGAGAG TAAAACCTCTC TGTCAGGTAC ATCTGGCTTT CTGTCCCAGC TCTGTCACTT 3360
AACACTTAGT TGCGGTGGGA AAACCTCCCTG ATCTTCCGGG AGACTAAGTA ACTGTATAAG 3420
CAAGCTGGCC GTGATATCCA CGTCGTAAGG CTGCTGTGTG GGTTCACTGA AAACGTGTTAC 3480
AGTGATTGGC AGAGTTCTG GAGGTCAATTG ACCCTCATTA AACCTTGCA ACACATTATTC 3540
TTACTACTCT TTGCTGTTAG TGTTGCCACC AGGATTGCCA TTCAAGGCAG TCCTGTATAC 3600
TTGATAACAC CAGTTGGTTC TGAGGCCTTA GTAGCATCT GTTAGCCTGG TTCAGGAGAG 3660
TGTATCAGAG CCAGGTTCCCT CTATCACATA AACTGTAACG CAAGTGAATT GTCCAATTGC 3720
TGTTGAGTCT GAGAGTCCTT GAGGTGCATA GCTTGACTA ATAAATCCCC ATGCTTTAT 3780
GCTTTCCCTT CCTCCCTCTT CCAGTTCAAC ATCTAATATA CAAAGATTGT TCCGACCACT 3840
ACGTGCTAGG AAGGAGAACG AGTGGGGCCT ACAGAGTTAC CCCTGATCAC AGAAACAGCA 3900
GCTTTGAGGT CTACTGTGAC ATGGAGACCA TGGGTGGAGG CTGGACGGTG CTGCAGGCTC 3960
GCCTTGATGG CAGCACCAAC TTCACCAGAG AGTGGAAAGA CTACAAAGCC GGCTTGAA 4020
ACCTTGAACG AGAATTTCGG TTGGGCAACG ATAAAATTCA TCTTCTGACC AAGAGTAAGG 4080
AAATGATTGTT GAGAATAGAT CTTGAAGACT TTAATGGTCT CACACTTAT GCCTTGTATG 4140
ATCAGTTTA TGTGGCTAAT GAATTCTCA AATACCGATT ACACATCGGT AACTACAATG 4200
GCACGGCAGG GGATGCCTTG CGTTTCAGTC GACACTACAA CCATGACCTG AGGTTTTCA 4260
CAACCCAGA CAGAGACAAAC GATCGGTACC CCTCTGGAA CTGTGGGCTC TATTACAGCT 4320

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CAGGCTGGTG GTTGATTCA TGTCTCTCTG CCAATTAAA TGGCAAATAT TACCACCAGA 4380
AATACAAAGG TGTCCGTAAT GGGATTCT GGGGCACCTG GCCTGGTATA AACCAAGGCAC 4440
AGCCAGGTGG CTACAAGTCC TCCTTCAAAC AGGCCAAGAT GATGATTAGG CCCAAGAATT 4500
TCAAGCCATA AATTGCTAGT GTTCATCTCT CTGGGCACTC ACTATCTAAG AGGACGATGA 4560
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CCTTTAAAGC TTTACAGCTT TTAGAATAAA GCTGAAAAGA TCTAAAAAGA CTCCTATGTT 4680
GCTGTTATAT GAGGAATGCT TGAAAGCACT GGAAATATTG ACAATTATAC ATTATAATTG 4740
CAAAACCTTT CATTTTATT AGTGAAAAG TTTCTAATA TTTTTATTAT TTTTATAATA 4800
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AAATATACAC ATTTGAGAAT ATACCAGTCC TTCCAGGTAC AACTGAAAGC CAAGAACTGT 4920
AGTATTATCT TTCGTCTAAG AAGAACTTAA AGCATTCTAG TTCTCAAGAA GAAGGGCAGG 4980
GATGGGATTG GGGGCCAGGG ACAATATGTA TAGCTAAATG TATTCTCTA ATGCAAAATA 5040
TGGCATTAAA ATACCTAAAA ATGTGGTAGC ATAATATATG TCTCTCCCT CTCCAATTGA 5100
AAAATAATGT TACCCTGTAG ACTTTGGTTT AGTGGTAATT CACTTACTGT TTATAGCCTG 5160
TTAGACCGCG ATACAAAAGC TGCTTATCC TCTCCCTCTG CTCTCTGTGC ACAATGGTTT 5220
GTGATGTAAG GTGCTAGACT ACTGTAAGGT TTCCTGGGG AAAGGCATGG TAAGGGAAAA 5280
CACACTGGTT TATATTGTA AAGCCAATCC TAATCCAAA GCAATACTGT TGTCGAGGAG 5340
TCAACGTTCT AGGAAGCTGA CTTTCTAGA ACAAAATGTAT TTATTAGGAT GAATTGGGA 5400
ATT 5403

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Arg Leu Pro Gly Trp Leu Trp Leu Ser Ser Ala Val Leu Ala Ala
1 5 10 15

Cys Arg Ala Val Glu Glu His Asn Leu Thr Glu Gly Leu Glu Asp Ala
20 25 30

Ser Ala Gln Ala Ala Cys Pro Ala Arg Leu Glu Gly Ser Gly Arg Cys
35 40 45

Glu Gly Ser Gln Cys Pro Phe Gln Leu Thr Leu Pro Thr Leu Thr Ile
50 55 60

Gln Leu Pro Arg Gln Leu Gly Ser Met Glu Glu Val Leu Lys Glu Val
55 70 75 80

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Arg Thr Leu Lys Glu Ala Val Asp Ser Leu Lys Lys Ser Cys Gln Asp
85 90 95

Cys Lys Leu Gln Ala Asp Asp His Arg Asp Pro Gly Gly Asn Gly Gly
100 105 110

Asn Gly Ala Glu Thr Ala Glu Asp Ser Arg Val Gln Glu Leu Glu Ser
115 120 125

Gln Val Asn Lys Leu Ser Ser Glu Leu Lys Asn Ala Lys Asp Gln Ile
130 135 140

Gln Gly Leu Gln Gly Arg Leu Glu Thr Leu His Leu Val Asn Met Asn
145 150 155 160

Asn Ile Glu Asn Tyr Val Asp Asn Lys Val Ala Asn Leu Thr Val Val
165 170 175

Val Asn Ser Leu Asp Gly Lys Cys Ser Lys Cys Pro Ser Gln Glu His
180 185 190

Met Gln Ser Gln Pro Val Gln His Leu Ile Tyr Lys Asp Cys Ser Asp
195 200 205

His Tyr Val Leu Gly Arg Arg Ser Ser Gly Ala Tyr Arg Val Thr Pro
210 215 220

Asp His Arg Asn Ser Ser Phe Glu Val Tyr Cys Asp Met Glu Thr Met
225 230 235 240

Gly Gly Gly Trp Thr Val Leu Gln Ala Arg Leu Asp Gly Ser Thr Asn
245 250 255

Phe Thr Arg Glu Trp Lys Asp Tyr Lys Ala Gly Phe Gly Asn Leu Glu
260 265 270

Arg Glu Phe Trp Leu Gly Asn Asp Lys Ile His Leu Leu Thr Lys Ser
275 280 285

Lys Glu Met Ile Leu Arg Ile Asp Leu Glu Asp Phe Asn Gly Leu Thr
290 295 300

Leu Tyr Ala Leu Tyr Asp Gln Phe Tyr Val Ala Asn Glu Phe Leu Lys
305 310 315 320

Tyr Arg Leu His Ile Gly Asn Tyr Asn Gly Thr Ala Gly Asp Ala Leu
325 330 335

Arg Phe Ser Arg His Tyr Asn His Asp Leu Arg Phe Phe Thr Thr Pro
340 345 350

Asp Arg Asp Asn Asp Arg Tyr Pro Ser Gly Asn Cys Gly Leu Tyr Tyr
355 360 365

Ser Ser Gly Trp Trp Phe Asp Ser Cys Leu Ser Ala Asn Leu Asn Gly
370 375 380

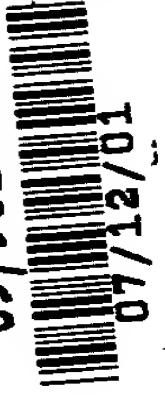
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385 390 395 400

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<223> n is any nucleic acid

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14. *How to use a computer to make a presentation* 300

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<213> Homo sapiens

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<400> 16

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<210> 17

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<223> Primer

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